Package 'BBI'

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Type Package

Title Benthic Biotic Indices Calculation from Composition Data

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Depends vegan

Description Set of functions to calculate Benthic Biotic Indices from composition data, obtained whether from morphotaxonomic inventories or sequencing data. Based on reference ecological weights publicly available for a set of commonly used marine biotic indices, such as AMBI (A Marine Biotic Index, Borja et al., 2000) <doi:10.1016/S0025-326X(00)00061-8> NSI (Norwegian Sensitivity Index) and ISI (Indicator Species Index) (Rygg 2013, <ISBN:978-82-577-6210-0>). It provides the ecological quality status of the samples based on each BBI as well as the normalized Ecological Quality Ratio.

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Encoding UTF-8

BugReports https://github.com/trtcrd/BBI/issues

URL https://github.com/trtcrd/BBI

NeedsCompilation no

Repository CRAN

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Contents

BBI *BBI*

Description

The BBI function searches the taxa of the composition data in the reference table for match. The taxonomic assignement usually includes previous taxonomic ranks, e.g. Kingdom;Phylum;Class;Order;Family;Genus;species. The taxonomic path must be separated by a semicolon ';' in order properly parsed by the function. The BBI function then compute benthic biotic indices. The function BBI returns a list of containing.

Usage

```
BBI(data, log = FALSE)
```

Arguments

data	A data frame containing samples as columns and taxa as rows, with species (or last taxonomic rank) in the first column
log	Whether or not keeping the history of match searching in a separate file in the workinf directory. Default = F

Value

Function BBI returns a list containing :

found	The amount of taxa that matched an entry in the database and the amount that did not.
BBI	The BBI values per sample.
table	The subset of composition data that contains only taxa with at least a match in one of the BBI.
taxa	The list of taxa that matched an entry and the correspondant OTU, if from metabarcoding data data.

References

Borja, A., Franco, J., Pérez, V., 2000. A Marine Biotic Index to Establish the Ecological Quality of Soft-Bottom Benthos Within European Estuarine and Coastal Environments. *Mar. Pollut. Bull.* 40, 1100–1114. doi:10.1016/S0025-326X(00)00061-8

Rygg, B., 2013. Norwegian Sensitivity Index (NSI) for marine macroinvertebrates, and an update of Indicator Species Index (ISI). *Norwegian Institute for Water Research*

Rygg, B., 2002. Indicator species index for assessing benthic ecological quality in marine waters of Norway. *Norwegian Institute for Water Research*

Examples

```
## Loading the exemple data
data("metab")
data("morpho")
## Computing BBI indices
BI_metab <- BBI(metab)
BI_morpho <- BBI(morpho)
## print values
BI_metab$BBI
## print classes
BI_metab$BBIclass
```

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metab *Subset of metabarcoding data*

Description

The metab dataset is an example of OTU table produced from metabarcoding data. OTUs are in rows and samples are in columns. It contains taxonomic assignements of OTUs in the first column. These assignement usually includes previous taxonomic ranks, e.g. Kingdom;Phylum;Class;Order;Family;Genus;species The taxonomic path must be separated by a semicolon ';' in order the properly parse it.

Usage

```
data("metab")
```

Examples

```
## Loading the exemple data
data("metab")
## Computing BBI indices
BI_metab <- BBI(metab)
## And then computing nEQR
eqr <- nEQR(BI_metab$BBI)
## print nEQR values
eqr$nEQR
## print discrete status
eqr$nEQRclass
```

morpho *Subset of morphologic inventories data*

Description

The morpho dataset is an example of morpho-taxonomic inventories table produced from microscopical analysis. Taxa are in rows and samples are in columns. It contains taxonomic assignements of taxa in the first column.

Usage

```
data("morpho")
```

Examples

```
## Loading the exemple data
data("morpho")
## Computing BBI indices
BI_morpho <- BBI(morpho)
## And then computing nEQR
eqr <- nEQR(BI_morpho$BBI)
## print nEQR values
eqr$nEQR
## print discrete status
eqr$nEQRclass
```

nEQR *nEQR*

Description

The nEQR function compute the normalized Ecological Quality Ratio (nEQR).

Usage

```
nEQR(data)
```

Arguments

data	A data frame containing samples as rows and BBI values as columns

Value

Function nEQR returns a list containing :

nEQR	The nEQR value.
nEQR_class	The dicrete ecological quality assessment.

Examples

```
## Loading the exemple data
data("metab")
data("morpho")
## Computing BBI indices
BI_metab <- BBI(metab)
BI_morpho <- BBI(morpho)
## And then computing nEQR
eqr <- nEQR(BI_metab$BBI)
## print nEQR values
eqr$nEQR
## print discrete status
eqr$nEQRclass
```

Index